



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

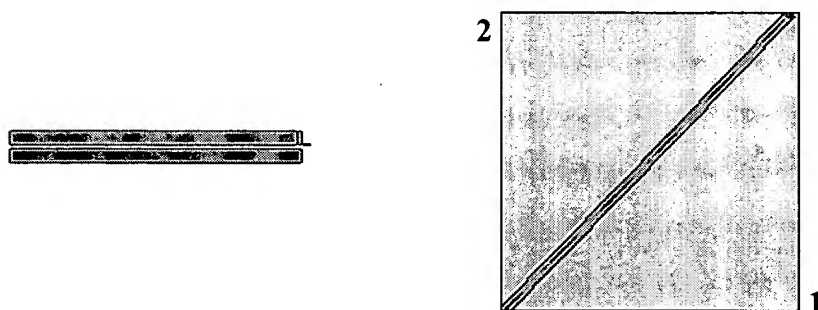
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.15 [Oct-15-2006]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☐ View option
 Masking character option ☒ X for protein, n for nucleotide Masking color option
☐ Show CDS translation

Sequence 1: lcl|seq_1
 Length = 9399 (1 .. 9399)

Sequence 2: gi|765144|gb|U22304.1|HGU22304Hepatitis GB virus B polypeptide complete genome.
 Length = 9143 (1 .. 9143)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.



Score = 1.732e+04 bits (9009), Expect = 0.0
 Identities = 9096/9137 (99%), Gaps = 4/9137 (0%)
 Strand=Plus/Plus

Query	1	ACCACAAACACTCCAGTTTGTACACTCCGCTAGGAATGCTCCTGGAGCACCCCCCTAG	60
Sbjct	1	ACCACAAACACTCCAGTTTGTACACTCCGCTAGGAATGCTCCTGGAGCACCCCCCTAG	60
Query	61	CAGGGCGTGGGGGATTTCCCCTGCCCGTCTGCAGAAGGGTGGAGCCAACCACCTTAGTAT	120
Sbjct	61	CAGGGCGTGGGGGATTTCCCCTGCCCGTCTGCAGAAGGGTGGAGCCAACCACCTTAGTAT	120
Query	121	GTAGGCGGCGGGACTCATGACGCTCGCGTGATGACAAGCGCCAAGCTTGACTTGGATGGC	180

Sbjct	121	GTAGGCGGCGGGACTCATGACGCTCGCGTGATGACAAGCGCCAAGCTTGACTTGGATGGC	180
Query	181	CCTGATGGGCGTTTCATGGGTTTCGGTGGTGGTGGCGCTTTAGGCAGCCTCCACGCCCACCA	240
Sbjct	181	CCTGATGGGCGTTTCATGGGTTTCGGTGGTGGTGGCGCTTTAGGCAGCCTCCACGCCCACCA	240
Query	241	CCTCCCAGATAGAGCGGCGGCACTGTAGGGAAGACCGGGGACCGGTCACTACCAAGGACG	300
Sbjct	241	CCTCCCAGATAGAGCGGCGGCACTGTAGGGAAGACCGGGGACCGGTCACTACCAAGGACG	300
Query	301	CAGACCTCTTTTTGAGTATCACGCCTCCGGAAGTAGTTGGGCAAGCCCACCTATATGTGT	360
Sbjct	301	CAGACCTCTTTTTGAGTATCACGCCTCCGGAAGTAGTTGGGCAAGCCCACCTATATGTGT	360
Query	361	TGGGATGGTTGGGGTTAGCCATCCATACCGTACTGCCTGATAGGGTCCTTGCGAGGGGAT	420
Sbjct	361	TGGGATGGTTGGGGTTAGCCATCCATACCGTACTGCCTGATAGGGTCCTTGCGAGGGGAT	420
Query	421	CTGGGAGTCTCGTAGACCGTAGCACATGCCTGTTATTTCTACTCAAACAAGTCCTGTACC	480
Sbjct	421	CTGGGAGTCTCGTAGACCGTAGCACATGCCTGTTATTTCTACTCAAACAAGTCCTGTACC	480
Query	481	TGCGCCAGAACGCGCAAGAACAAGCAGACGCAGGCTTCATATCCTGTGTCCATTAAAAC	540
Sbjct	481	TGCGCCAGAACGCGCAAGAACAAGCAGACGCAGGCTTCATATCCTGTGTCCATTAAAAC	540
Query	541	ATCTGTTGAAAGGGGACAACGAGCAAAGCGCAAAGTCCAGCGCGATGCTCGGCCTCGTAA	600
Sbjct	541	ATCTGTTGAAAGGGGACAACGAGCAAAGCGCAAAGTCCAGCGCGATGCTCGGCCTCGTAA	600
Query	601	TTACAAAATTGCTGGTATCCATGATGGCTTGCAGACATTGGCTCAGGCTGCTTTGCCAGC	660
Sbjct	601	TTACAAAATTGCTGGTATCCATGATGGCTTGCAGACATTGGCTCAGGCTGCTTTGCCAGC	660
Query	661	TCATGGTTGGGGACGCCAAGACCCTCGCCATAAGTCTCGCAATCTTGGAATCCTTCTGGA	720
Sbjct	661	TCATGGTTGGGGACGCCAAGACCCTCGCCATAAGTCTCGCAATCTTGGAATCCTTCTGGA	720
Query	721	TTACCCTTTGGGGTGGATTGGTGATGTTACAACCTCACACACCTCTAGTAGGCCCGCTGGT	780
Sbjct	721	TTACCCTTTGGGGTGGATTGGTGATGTTACAACCTCACACACCTCTAGTAGGCCCGCTGGT	780
Query	781	GGCAGGAGCGGTCGTTTCGACCAGTCTGCCAGATAGTACGCTTGCTGGAGGATGGAGTCAA	840
Sbjct	781	GGCAGGAGCGGTCGTTTCGACCAGTCTGCCAGATAGTACGCTTGCTGGAGGATGGAGTCAA	840
Query	841	CTGGGCTACTGGTTGGTTCGGTGTCCACCTTTTTGTGGTATGTCTGCTATCTTTGGCCTG	900
Sbjct	841	CTGGGCTACTGGTTGGTTCGGTGTCCACCTTTTTGTGGTATGTCTGCTATCTTTGGCCTG	900
Query	901	TCCCTGTAGTGGGGCGCGGGTCACTGACCCAGACACAAATACCACAATCCTGACCAATTG	960
Sbjct	901	TCCCTGTAGTGGGGCGCGGGTCACTGACCCAGACACAAATACCACAATCCTGACCAATTG	960
Query	961	CTGCCAGCGTAATCAGGTTATCTATTGTTCTCCTTCCACTTGCCTACACGAGCCTGGTTG	1020
Sbjct	961	CTGCCAGCGTAATCAGGTTATCTATTGTTCTCCTTCCACTTGCCTACACGAGCCTGGTTG	1020
Query	1021	TGTGATCTGTGCGGACGAGTGCTGGGTTCCCGCCAATCCGTACATCTCACACCCTTCCAA	1080

Sbjct	1021	TGTGATCTGCGCGGACGAGTGCTGGGTTCCCGCCAATCCGTACATCTCACACCCTTCCAA	1080
Query	1081	TTGGACTGGCACGGACTCCTTCTTGGCTGACCACATTGATTTTGTATGGGCGCTCTTGT	1140
Sbjct	1081	TTGGACTGGCACGGACTCCTTCTTGGCTGACCACATTGATTTTGTATGGGCGCTCTTGT	1140
Query	1141	GACCTGTGACGCCCTTGACATTGGTGAGTTGTGTGGTGCGTGTGTATTAGTCGGTGACTG	1200
Sbjct	1141	GACCTGTGACGCCCTTGACATTGGTGAGTTGTGTGGTGCGTGTGTATTAGTCGGTGACTG	1200
Query	1201	GCTTGTGAGGCACTGGCTTATTCACATAGACCTCAATGAACTGGTACTTGTTACCTGGA	1260
Sbjct	1201	GCTTGTGAGGCACTGGCTTATTCACATAGACCTCAATGAACTGGTACTTGTTACCTGGA	1260
Query	1261	AGTGCCCACTGGAATAGATCCTGGGTTCTAGGGTTTATCGGGTGGATGGCCGGCAAGGT	1320
Sbjct	1261	AGTGCCCACTGGAATAGATCCTGGGTTCTAGGGTTTATCGGGTGGATGGCCGGCAAGGT	1320
Query	1321	CGAGGCTGTCATCTTCTTGACCAAAGTGGCTTCACAAGTACCATACGCTATTGCGACTAT	1380
Sbjct	1321	CGAGGCTGTCATCTTCTTGACCAAAGTGGCTTCACAAGTACCATACGCTATTGCGACTAT	1380
Query	1381	GTTTAGCAGTGTACACTACCTGGCGGTTGGCGCTCTGATCTACTATGCCTCTCGGGGCAA	1440
Sbjct	1381	GTTTAGCAGTGTACACTACCTGGCGGTTGGCGCTCTGATCTACTATGCCTCTCGGGGCAA	1440
Query	1441	GTGGTATCAGTTGCTCCTAGCGCTTATGCTTTACATAGAAGCGACCTCTGGAAACCTAT	1500
Sbjct	1441	GTGGTATCAGTTGCTCCTAGCGCTTATGCTTTACATAGAAGCGACCTCTGGAAACCTAT	1500
Query	1501	CAGGGTGCCCACTGGATGCTCAATAGCTGAGTTTTGCTCGCCTTTGATGATACCATGTCC	1560
Sbjct	1501	CAGGGTGCCCACTGGATGCTCAATAGCTGAGTTTTGCTCGCCTTTGATGATACCATGTCC	1560
Query	1561	TTGCCACTCTTATTTGAGTGAGAATGTGTCAGAAGTCATTTGTTACAGTCCAAAGTGGAC	1620
Sbjct	1561	TTGCCACTCTTATTTGAGTGAGAATGTGTCAGAAGTCATTTGTTACAGTCCAAAGTGGAC	1620
Query	1621	CAGGCCTATCACTCTAGAGTATAACAACCTCCATATCTTGGTACCCCTATACAATCCCTGG	1680
Sbjct	1621	CAGGCCTATCACTCTAGAGTATAACAACCTCCATATCTTGGTACCCCTATACAATCCCTGG	1680
Query	1681	TGCGAGGGGATGTATGGTTAAATTCAAAAATAACACATGGGGTTGCTGCCGTATTCGCAA	1740
Sbjct	1681	TGCGAGGGGATGTATGGTTAAATTCAAAAATAACACATGGGGTTGCTGCCGTATTCGCAA	1740
Query	1741	TGTGCCATCGTACTGCACTATGGGCACTGATGCAGTGTGGAACGACACTCGCAACACTTA	1800
Sbjct	1741	TGTGCCATCGTACTGCACTATGGGCACTGATGCAGTGTGGAACGACACTCGCAACACTTA	1800
Query	1801	CGAAGTATGCGGTGTAACACCATGGCTAACAACCGCATGGCACAACGGCTCAGCCCTGAA	1860
Sbjct	1801	CGAAGCATGCGGTGTAACACCATGGCTAACAACCGCATGGCACAACGGCTCAGCCCTGAA	1860
Query	1861	ATTGGCTATATTACAATACCCTGGGTCTAAAGAAATGTTTAAACCTCATAATTGGATGTC	1920
Sbjct	1861	ATTGGCTATATTACAATACCCTGGGTCTAAAGAAATGTTTAAACCTCATAATTGGATGTC	1920
Query	1921	AGGCCATTTGTATTTTGAGGGATCAGATACCCCTATAGTTTACTTTTATGACCCTGTGAA	1980

Sbjct	1921	AGGCCATTTGTATTTTGGAGGGATCAGATACCCCTATAGTTTACTTTTATGACCCTGTGAA	1980
Query	1981	TTCCACTCTCCTACCACCGGAGAGGTGGGCTAGGTTGCCCGGTACCCACCTGTGGTACG	2040
Sbjct	1981	TTCCACTCTCCTACCACCGGAGAGGTGGGCTAGGTTGCCCGGTACCCACCTGTGGTACG	2040
Query	2041	TGGTTCTTGGTTACAGGTTCCGCAAGGGTTTTACAGTGATGTGAAAGACCTAGCCACAGG	2100
Sbjct	2041	TGGTTCTTGGTTACAGGTTCCGCAAGGGTTTTACAGTGATGTGAAAGACCTAGCCACAGG	2100
Query	2101	ATTGATCACCAAAGACAAAGCCTGGAAAAATTATCAGGTCTTATATTCCGCCACGGGTGC	2160
Sbjct	2101	ATTGATCACCAAAGACAAAGCCTGGAAAAATTATCAGGTCTTATATTCCGCCACGGGTGC	2160
Query	2161	TTTGTCTCTTACGGGAGTTACCACCAAGGCCGTGGTGCTAATTCTGTTGGGGTTGTGTGG	2220
Sbjct	2161	TTTGTCTCTTACGGGAGTTACCACCAAGGCCGTGGTGCTAATTCTGTTGGGGTTGTGTGG	2220
Query	2221	CAGCAAGTATCTTATTTTAGCCTACCTCTGTTACTTGTCCCTTTGTTTTGGGCGCGCTTC	2280
Sbjct	2221	CAGCAAGTATCTTATTTTAGCCTACCTCTGTTACTTGTCCCTTTGTTTTGGGCGCGCTTC	2280
Query	2281	TGGTTACCCTTTGCGTCTGTGCTCCCATCCCAGTCGTATCTCCAAGCTGGCTGGGATGT	2340
Sbjct	2281	TGGTTACCCTTTGCGTCTGTGCTCCCATCCCAGTCGTATCTCCAAGCTGGCTGGGATGT	2340
Query	2341	TTTGTCTAAAGCTCAAGTAGCTCCTTTTGCTTTGATTTTCTTCATCTGTTGCTATCTCCG	2400
Sbjct	2341	TTTGTCTAAAGCTCAAGTAGCTCCTTTTGCTTTGATTTTCTTCATCTGTTGCTATCTCCG	2400
Query	2401	CTGCAGGCTACGTTATGCTGCCCTTTTAGGGTTTGTGCCCATGGCTGCGGGCTTGCCCCT	2460
Sbjct	2401	CTGCAGGCTACGTTATGCTGCCCTTTTAGGGTTTGTGCCCATGGCTGCGGGCTTGCCCCT	2460
Query	2461	AACTTTCTTTGTTGCAGCAGCTGCTGCCCAACCAGATTATGACTGGTGGGTGCGACTGCT	2520
Sbjct	2461	AACTTTCTTTGTTGCAGCAGCTGCTGCCCAACCAGATTATGACTGGTGGGTGCGACTGCT	2520
Query	2521	AGTGGCAGGGTTAGTTTTGTGGGCCGGCCGTAACCGTGGTCACCGCATAGCTCTGCTTGT	2580
Sbjct	2521	AGTGGCAGGGTTAGTTTTGTGGGCCGGCCGTAACCGTGGTCACCGCATAGCTCTGCTTGT	2580
Query	2581	AGGTCCTTGGCCTCTGGTAGCGCTTTTAACCCTCTTGCATTTGGTTACGCCTGCTTCAGC	2640
Sbjct	2581	AGGTCCTTGGCCTCTGGTAGCGCTTTTAACCCTCTTGCATTTGGTTACGCCTGCTTCAGC	2640
Query	2641	TTTTGATACCGAGATAATTGGAGGGCTGACAATACCACCTGTAGTAGCATTAGTTGTCAT	2700
Sbjct	2641	TTTTGATACCGAGATAATTGGAGGGCTGACAATACCACCTGTAGTAGCATTAGTTGTCAT	2700
Query	2701	GTCTCGTTTTGGCTTCTTTGCTCACTTGTTACCTCGCTGTGCTTTAGTTAACTCCTATCT	2760
Sbjct	2701	GTCTCGTTTTGGCTTCTTTGCTCACTTGTTACCTCGCTGTGCTTTAGTTAACTCCTATCT	2760
Query	2761	TTGGCAACGTTGGGAGAATTGGTTTTGGAACGTTACACTAAGACCGGAGAGGTTTTCTCCT	2820
Sbjct	2761	TTGGCAACGTTGGGAGAATTGGTTTTGGAACGTTACACTAAGACCGGAGAGGTTTTCTCCT	2820
Query	2821	TGTGCTGGTTTTGTTTTCCCGGTGCGACATATGACGCGCTGGTGACTTTCTGTGTGTGTCA	2880

Sbjct	2821	TGTGCTGGTTTGTTCCTCCCGGTGCGACATATGACACGCTGGTGACTTTCTGTGTGTGTCA	2880
Query	2881	CGTAGCTCTTCTATGTTTAAACATCCAGTGCAGCATCGTTCTTTGGGACTGACTCTAGGGT	2940
Sbjct	2881	CGTAGCTCTTCTATGTTTAAACATCCAGTGCAGCATCGTTCTTTGGGACTGACTCTAGGGT	2940
Query	2941	TAGGGCCCATAGAATGTTGGTGCGTCTCGGAAAGTGTCATGCTTGGTATTCTCATTATGT	3000
Sbjct	2941	TAGGGCCCATAGAATGTTGGTGCGTCTCGGAAAGTGTCATGCTTGGTATTCTCATTATGT	3000
Query	3001	TCTTAAGTTTTTCTCTTAGTGTTTGGTGAGAATGGTGTGTTTTTCTATAAGCACTTGCA	3060
Sbjct	3001	TCTTAAGTTTTTCTCTTAGTGTTTGGTGAGAATGGTGTGTTTTTCTATAAGCACTTGCA	3060
Query	3061	TGGTGATGTCTTGCCTAATGATTTTGCCTCGAAACTACCATTGCAAGAGCCATTTTTCCC	3120
Sbjct	3061	TGGTGATGTCTTGCCTAATGATTTTGCCTCGAAACTACCATTGCAAGAGCCATTTTTCCC	3120
Query	3121	TTTTGAAGGCAAGGCAAGGGTCTATAGGAATGAAGGAAGACGCTTGGCGTGTGGGGACAC	3180
Sbjct	3121	TTTTGAAGGCAAGGCAAGGGTCTATAGGAATGAAGGAAGACGCTTGGCGTGTGGGGACAC	3180
Query	3181	GGTTGATGGTTTGGCCGTTGTTGCGCGTCTCGGCGACCTTGTTTTCGCAGGGTTGGCTAT	3240
Sbjct	3181	GGTTGATGGTTTGGCCGTTGTTGCGCGTCTCGGCGACCTTGTTTTCGCAGGGTTAGCTAT	3240
Query	3241	GCCGCCAGATGGGTGGGCCATTACCGCACCTTTTACGCTGCAGTGTCTCTCTGAACGTGG	3300
Sbjct	3241	GCCGCCAGATGGGTGGGCCATTACCGCACCTTTTACGCTGCAGTGTCTCTCTGAACGTGG	3300
Query	3301	CACGCTGTCTAGCGATGGCAGTGGTCATGACTGGTATAGACCCCGAACTTGGACTGGAAC	3360
Sbjct	3301	CACGCTGTCTAGCGATGGCAGTGGTCATGACTGGTATAGACCCCGAACTTGGACTGGAAC	3360
Query	3361	TATCTTCAGATTAGGATCTCTGGCCACTAGCTACATGGGATTTGTTTGTGACAACGTGTT	3420
Sbjct	3361	TATCTTCAGATTAGGATCTCTGGCCACTAGCTACATGGGATTTGTTTGTGACAACGTGTT	3420
Query	3421	GTATACTGCTCACCATGGCAGCAAGGGGCGCCGGTTGGCTCATCCACAGGCTCTATACA	3480
Sbjct	3421	GTATACTGCTCACCATGGCAGCAAGGGGCGCCGGTTGGCTCATCCACAGGCTCCATACA	3480
Query	3481	CCCAATAACCGTTGACGCGGCTAATGACCAGGACATCTATCAACCACCATGTGGAGCTGG	3540
Sbjct	3481	CCCAATAACCGTTGACGCGGCTAATGACCAGGACATCTATCAACCACCATGTGGAGCTGG	3540
Query	3541	GTCCCTTACTCGGTGCTCTTGCGGGGAGACCAAGGGGTATCTGGTAACACGACTGGGGTC	3600
Sbjct	3541	GTCCCTTACTCGGTGCTCTTGCGGGGAGACCAAGGGGTATCTGGTAACACGACTGGGGTC	3600
Query	3601	ATTGGTTGAGGTCAACAAATCCGATGACCCTTATTGGTGTGTGTGCGGGGCCCTTCCCAT	3660
Sbjct	3601	ATTGGTTGAGGTCAACAAATCCGATGACCCTTATTGGTGTGTGTGCGGGGCCCTTCCCAT	3660
Query	3661	GGCTGTTGCCAAGGGTTCTTCAGGTGCCCCGATTCTGTGCTCCTCCGGGCATGTTATTGG	3720
Sbjct	3661	GGCTGTTGCCAAGGGTTCTTCAGGTGCCCCGATTCTGTGCTCCTCCGGGCATGTTATTGG	3720
Query	3721	GATGTTACCGCTGCTAGAAATTCTGGCGGTTGAGTCAGTCAGATTAGGGTTAGGCCGTT	3780

Sbjct	3721	GATGTTACCGCTGCTAGAAATTCTGGCGGTTCAAGTCAGCCAGATTAGGGTTAGGCCGTT	3780
Query	3781	GGTGTGTGCTGGATACCATCCCCAGTACACAGCACATGCCACTCTTGATACAAAACCTAC	3840
Sbjct	3781	GGTGTGTGCTGGATACCATCCCCAGTACACAGCACATGCCACTCTTGATACAAAACCTAC	3840
Query	3841	TGTGCCTAACGAGTATTCAAGTGCAAATTTTAATTGCCCCCACTGGCAGCGGCAAGTCAAC	3900
Sbjct	3841	TGTGCCTAACGAGTATTCAAGTGCAAATTTTAATTGCCCCCACTGGCAGCGGCAAGTCAAC	3900
Query	3901	CAAATTACCACTTTCTTACATGCAGGAGAAGTATGAGGTCTTGGTCCTAAATCCCAGTGT	3960
Sbjct	3901	CAAATTACCACTTTCTTACATGCAGGAGAAGTATGAGGTCTTGGTCCTAAATCCCAGTGT	3960
Query	3961	GGCTACAACAGCATCAATGCCAAAGTACATGCACGCGACGTACGGCGTGAATCCAAATTG	4020
Sbjct	3961	GGCTACAACAGCATCAATGCCAAAGTACATGCACGCGACGTACGGCGTGAATCCAAATTG	4020
Query	4021	CTATTTTAATGGCAAATGTACCAACACAGGGGCTTCACTTACGTACAGCACATATGGCAT	4080
Sbjct	4021	CTATTTTAATGGCAAATGTACCAACACAGGGGCTTCACTTACGTACAGCACATATGGCAT	4080
Query	4081	GTACCTGACCGGAGCATGTTCCCGGAACATGATGTAATCATTGTGACGAATGCCATGC	4140
Sbjct	4081	GTACCTGACCGGAGCATGTTCCCGGAACATGACGTCATCATTGTGACGAATGCCATGC	4140
Query	4141	TACCGATGCAACCACCGTGTTGGGCATTGGAAAGGTCTAACCGAAGCTCCATCCAAAAA	4200
Sbjct	4141	TACCGATGCAACCACCGTGTTGGGCATTGGAAAGGTCTAACCGAAGCTCCATCCAAAAA	4200
Query	4201	TGTTAGGCTAGTGGTTCTTGCCACGGCTACCCCCCTGGAGTAATCCCTACACCACATGC	4260
Sbjct	4201	TGTTAGGCTAGTGGTTCTTGCCACGGCTACCCCCCTGGAGTAATCCCTACACCACATGC	4260
Query	4261	CAACATAACTGAGATTCAATTAACCGATGAAGGCACTATCCCCTTTTCATGGAAAAAAGAT	4320
Sbjct	4261	CAACATAACTGAGATTCAATTAACCGATGAAGGCACTATCCCCTTTTCATGGAAAAAAGAT	4320
Query	4321	TAAGGAGGAAAATCTGAAGAAAGGGAGACACCTTATCTTTGAGGCTACCAAAAAACACTG	4380
Sbjct	4321	TAAGGAGGAAAATCTGAAGAAAGGGAGACACCTTATCTTTGAGGCTACCAAAAAACACTG	4380
Query	4381	TGATGAGCTTGCTAACGAGTTAGCTCGAAAGGGAATAACAGCTGTCTCTTACTATAGGGG	4440
Sbjct	4381	TGATGAGCTTGCTAACGAGTTAGCTCGAAAGGGAATAACAGCTGTCTCTTACTATAGGGG	4440
Query	4441	ATGTGACATCTCAAAAATCCCTGAGGGCGACTGTGTAGTAGTTGCCACTGATGCCTTGTG	4500
Sbjct	4441	ATGTGACATCTCAAAAATCCCTGAGGGCGACTGTGTAGTAGTTGCCACTGATGCCTTGTG	4500
Query	4501	TACAGGGTACACTGGTGACTTTGATTCCGTGTATGACTGCAGCCTCATGGTAGAAGGCAC	4560
Sbjct	4501	TACAGGGTACACTGGTGACTTTGATTCCGTGTATGACTGCAGCCTCATGGTAGAAGGCAC	4560
Query	4561	ATGCCATGTTGACCTTGACCCTACTTTACCATGGGTGTTTCGTGTGTGCGGGGTTTCAGC	4620
Sbjct	4561	ATGCCATGTTGACCTTGACCCTACTTTACCATGGGTGTTTCGTGTGTGCGGGGTTTCAGC	4620
Query	4621	AATAGTTAAAGGCCAGCGTAGGGGCCGCACAGGCCGTGGGAGAGCTGGCATATACTACTA	4680

Sbjct	4621	AATAGTTAAAGGCCAGCGTAGGGGCCGCACAGGCCGTGGGAGAGCTGGCATATACTACTA	4680
Query	4681	TGTAGACGGGAGTTGTACCCCTTCGGGTATGGTTCCTGAATGCAACATTGTTGAAGCCTT	4740
Sbjct	4681	TGTAGACGGGAGTTGTACCCCTTCGGGTATGGTTCCTGAATGCAACATTGTTGAAGCCTT	4740
Query	4741	CGACGCAGCCAAGGCATGGTATGGTTTGTTCATCAACAGAAGCTCAAACATTCTGGACAC	4800
Sbjct	4741	CGACGCAGCCAAGGCATGGTATGGTTTGTTCATCAACAGAAGCTCAAACATTCTGGACAC	4800
Query	4801	CTATCGCACCCAACCTGGGTTACCTGCGATAGGAGCAAATTTGGACGAGTGGGCTGATCT	4860
Sbjct	4801	CTATCGCACCCAACCTGGGTTACCTGCGATAGGAGCAAATTTGGACGAGTGGGCTGATCT	4860
Query	4861	CTTTTCTATGGTCAACCCCGAACCTTCATTTGTCAATACTGCAAAAAGAACTGCTGACAA	4920
Sbjct	4861	CTTTTCTATGGTCAACCCCGAACCTTCATTTGTCAATACTGCAAAAAGAACTGCTGACAA	4920
Query	4921	TTATGTTTTGTTGACTGCAGCCCAACTACAACGTGTGTCATCAGTATGGCTATGCTGCTCC	4980
Sbjct	4921	TTATGTTTTGTTGACTGCAGCCCAACTACAACGTGTGTCATCAGTATGGCTATGCTGCTCC	4980
Query	4981	CAATGACGCACCACGGTGGCAGGGAGCCCGGCTTGGGAAAAACCTTGTGGGGTTCTGTG	5040
Sbjct	4981	CAATGACGCACCACGGTGGCAGGGAGCCCGGCTTGGGAAAAACCTTGTGGGGTTCTGTG	5040
Query	5041	GCGCTTGGACGGCGCTGACGCCTGTCCTGGCCCAGAGCCCAGCGAGGTGACCAGATACCA	5100
Sbjct	5041	GCGCTTGGACGGCGCTGACGCCTGTCCTGGCCCAGAGCCCAGCGAGGTGACCAGATACCA	5100
Query	5101	AATGTGCTTCACTGAAGTCAATACTTCTGGGACAGCCGCACTCGCTGTTGGCGTTGGAGT	5160
Sbjct	5101	AATGTGCTTCACTGAAGTCAATACTTCTGGGACAGCCGCACTCGCTGTTGGCGTTGGAGT	5160
Query	5161	GGCTATGGCTTATCTAGCCATTGACACTTTTGGCGCCACTTGTGTGCGGCGTTGCTGGTC	5220
Sbjct	5161	GGCTATGGCTTATCTAGCCATTGACACTTTTGGCGCCACTTGTGTGCGGCGTTGCTGGTC	5220
Query	5221	TATTGCATCAGTCCCTACCGGTGCTACTGTCGCCCCAGTGGTTGACGAAGAAGAAATCGT	5280
Sbjct	5221	TATTACATCAGTCCCTACCGGTGCTACTGTCGCCCCAGTGGTTGACGAAGAAGAAATCGT	5280
Query	5281	GGAGGAGTGTGCATCATTCATTCCCTTGGAGGCCATGGTTGCTGCAATCGATAAGCTGAA	5340
Sbjct	5281	GGAGGAGTGTGCATCATTCATTCCCTTGGAGGCCATGGTTGCTGCAATCGATAAGCTGAA	5340
Query	5341	GAGTACAATCACCACAACCTAGTCCTTTTACATTGGAAACCGCCCTTGAAAACTTAACAC	5400
Sbjct	5341	GAGTACAATAACCACAACCTAGTCCTTTTACATTGGAAACCGCCCTTGAAAACTTAACAC	5400
Query	5401	CTTTCTTGGGCCTCATGCAGCTACAATCCTTGCTATCATAGAGTATTGCTGTGGTTTAGT	5460
Sbjct	5401	CTTTCTTGGGCCTCATGCAGCTACAATCCTTGCTATCATAGAGTATTGCTGTGGCTTAGT	5460
Query	5461	CACTTTACCTGACAATCCCTTTGCATCATGCGTGTGCTTTTATTGCGGGTATTACTAC	5520
Sbjct	5461	CACTTTACCTGACAATCCCTTTGCATCATGCGTGTGCTTTTATTGCGGGTATTACTAC	5520
Query	5521	CCCACTACCTCACAAGATCAAAATGTTTCCTGTCATTATTTGGAGGCGCAATTGCGTCCAA	5580

Sbjct	5521	CCCACTACCTCACAAGATCAAAATGTTTCCTGTCATTATTTGGAGGCGCAATTGCGTCCAA	5580
Query	5581	GCTTACAGACGCTAGAGGCGCACTGGCGTTCATGATGGCCGGGGCTGCGGGAACAGCTCT	5640
Sbjct	5581	GCTTACAGACGCTAGAGGCGCACTGGCGTTCATGATGGCCGGGGCTGCGGGAACAGCTCT	5640
Query	5641	TGGTACATGGACATCGGTGGGTTTTGTCTTTGACATGCTAGGCGGCTATGCTGCCGCCTC	5700
Sbjct	5641	TGGTACATGGACATCGGTGGGTTTTGTCTTTGACATGCTAGGCGGCTATGCTGCCGCCTC	5700
Query	5701	ATCCACTGCTTGCTTGACATTTAAATGCTTGATGGGTGAGTGGCCCACTATGGATCAGCT	5760
Sbjct	5701	ATCCACTGCTTGCTTGACATTTAAATGCTTGATGGGTGAGTGGCCCACTATGGATCAGCT	5760
Query	5761	TGCTGGTTTAGTCTACTCCGCGTTCAATCCGGCCGCAGGAGTTGTGGGCGTCTTGTGAGC	5820
Sbjct	5761	TGCTGGTTTAGTCTACTCCGCGTTCAATCCGGCCGCAGGAGTTGTGGGCGTCTTGTGAGC	5820
Query	5821	TTGTGCAATGTTTGCTTTGACAACAGCAGGGCCAGATCACTGGCCCAACAGACTTCTTAC	5880
Sbjct	5821	TTGTGCAATGTTTGCTTTGACAACAGCAGGGCCAGATCACTGGCCCAACAGACTTCTTAC	5880
Query	5881	TATGCTTGCTAGGAGCAACACTGTATGTAATGAGTACTTTATTGCCACTCGTGACATCCG	5940
Sbjct	5881	TATGCTTGCTAGGAGCAACACTGTATGTAATGAGTACTTTATTGCCACTCGTGACATCCG	5940
Query	5941	CAGGAAGATACTGGGCATTCTGGAGGCATCTACCCCCTGGAGTGTGCATATCAGCTTGCAT	6000
Sbjct	5941	CAGGAAGATACTGGGCATTCTGGAGGCATCTACCCCCTGGAGTGTGCATATCAGCTTGCAT	6000
Query	6001	CCGTTGGCTCCACACCCCGACGGAGGATGATTGCGGCCTCATTGCTTGGGGTCTAGAGAT	6060
Sbjct	6001	CCGTTGGCTCCACACCCCGACGGAGGATGATTGCGGCCTCATTGCTTGGGGTCTAGAGAT	6060
Query	6061	TTGGCAGTATGTGTGCAATTTCTTTGTGATTTGCTTTAATGTCCTTAAAGCTGGAGTTCA	6120
Sbjct	6061	TTGGCAGTATGTGTGCAATTTCTTTGTGATTTGCTTTAATGTCCTTAAAGCTGGAGTTCA	6120
Query	6121	GAGCATGGTTAACATTCTGGTTGTCCTTTCTACAGCTGCCAGAAGGGGTACAAGGGCCC	6180
Sbjct	6121	GAGCATGGTTAACATTCTGGTTGTCCTTTCTACAGCTGCCAGAAGGGGTACAAGGGCCC	6180
Query	6181	CTGGATTGGATCAGGTATGCTCCAAGCACGCTGTCCATGCGGTGCTGAACTCATCTTTTC	6240
Sbjct	6181	CTGGATTGGATCAGGTATGCTCCAAGCACGCTGTCCATGCGGTGCTGAACTCATCTTTTC	6240
Query	6241	TGTTGAGAATGGTTTTGCAAACTTTACAAAGGACCCAGAAGTTGTTCAAATTACTGGAG	6300
Sbjct	6241	TGTTGAGAATGGTTTTGCAAACTTTACAAAGGACCCAGAAGTTGTTCAAATTACTGGAG	6300
Query	6301	AGGGGCTGTTCCAGTCAACGCTAGGCTGTGTGGGTGCGCTAGACCGGACCCAACTGATTG	6360
Sbjct	6301	AGGGGCTGTTCCAGTCAACGCTAGGCTGTGTGGGTGCGCTAGACCGGACCCAACTGATTG	6360
Query	6361	GACTAGTCTTGTCGTCAATTATGGCGTTAGGGACTACTGTAAATATGAGAAAATGGGAGA	6420
Sbjct	6361	GACTAGTCTTGTCGTCAATTATGGCGTTAGGGACTACTGTAAATATGAGAAAATGGGAGA	6420
Query	6421	TCACATTTTTGTTACAGCAGTATCCTCTCAAATGTCTGTTTCACCCAGGTGCCCCAAC	6480

Sbjct	6421	TCACATTTTTGTTACAGCAGTATCCTCTCCAAATGTCTGTTTCACCCAGGTGCCCCAAC	6480
Query	6481	CTTGAGAGCTGCAGTGGCCGTGGACGGCGTACAGGTTTACAGTGTATCTAGGTGAGCCCAA	6540
Sbjct	6481	CTTGAGAGCTGCAGTGGCCGTGGACGGCGTACAGGTTTACAGTGTATCTAGGTGAGCCCAA	6540
Query	6541	AACTCCTTGGACGACATCTGCTTGCTGTTACGGTCCTGACGGTAAGGGTAAAACGTGTTAA	6600
Sbjct	6541	AACTCCTTGGACGACATCTGCTTGCTGTTACGGTCCTGACGGTAAGGGTAAAACGTGTTAA	6600
Query	6601	GCTTCCCTTCCGCGTTGACGGTCACACACCTGGTGTGCGCATGCAACTTAATTTGCGTGA	6660
Sbjct	6601	GCTTCCCTTCCGCGTTGACGGTCACACACCTGGTGTGCGCATGCAACTTAATTTGCGTGA	6660
Query	6661	TGCACTTGAGACAAATGACTGTAATTCACAAACAACACTCCTAGTGATGAAGCCGCAGT	6720
Sbjct	6661	TGCACTTGAGACAAATGACTGTAATTCATAAACAACACTCCTAGTGATGAAGCCGCAGT	6720
Query	6721	GTCCGCTCTTGTTTTCAAACAGGAGTTGCGGCGTACAAACCAATTGCTTGAGGCAATTTT	6780
Sbjct	6721	GTCCGCTCTTGTTTTCAAACAGGAGTTGCGGCGTACAAACCAATTGCTTGAGGCAATTTT	6780
Query	6781	AGCTGGCGTTGACACCACCAAACCTGCCAGCCCCCTCCATCGAAGAGGTAGTGGTAAGAAA	6840
Sbjct	6781	AGCTGGCGTTGACACCACCAAACCTGCCAGCCCCCTCCATCGAAGAGGTAGTGGTAAGAAA	6840
Query	6841	GCGCCAGTTCCGGGCAAGAACTGGTTCGCTTACCTTGCCCTCCCCCTCCGAGATCCGTCCC	6900
Sbjct	6841	GCGCCAGTTCCGGGCAAGAACTGGTTCGCTTACCTTGCCCTCCCCCTCCGAGATCCGTCCC	6900
Query	6901	AGGAGTGTTCATGTCCTGAAAGCCTGCAACGAAGTGACCCGTTAGAAGGTCCTTCAAACCT	6960
Sbjct	6901	AGGAGTGTTCATGTCCTGAAAGCCTGCAACGAAGTGACCCGTTAGAAGGTCCTTCAAACCT	6960
Query	6961	CCCTCCTTCACCACCTGTTCTACAGTTGGCCATGCCGATGCCCTGTTGGGAGCGGGTGA	7020
Sbjct	6961	CCCTCCTTCACCACCTGTTCTACAGTTGGCCATGCCGATGCCCTGTTGGGAGCAGGTGA	7020
Query	7021	GTGTAACCCTTTCACTGCAATTGGATGTGCAATGACCGAAACAGGCGGAGGCCCTGATGA	7080
Sbjct	7021	GTGTAACCCTTTCACTGCAATTGGATGTGCAATGACCGAAACAGGCGGAGGCCCTGATGA	7080
Query	7081	TTTACCCAGTTACCCTCCCAAAAAGGAGGTCTCTGAATGGTCAGACGAAAGTTGGTCGAC	7140
Sbjct	7081	TTTACCCAGTTACCCTCCCAAAAAGGAGGTCTCTGAATGGTCAGACGAAAGTTGGTCAAC	7140
Query	7141	GGCTACAACCGTTTCCAGCTACGTTACTGGCCCCCGTACCCTAAGATACGGGGAAAGGA	7200
Sbjct	7141	GACTACAACCGCTTCCAGCTACGTTACTGGCCCCCGTACCCTAAGATACGGGGAAAGGA	7200
Query	7201	TTCCACTCAGTCAGCCCCCGCCAAACGGCCTACAAAAAGAAGTTGGGAAAGAGTGAGTT	7260
Sbjct	7201	TTCCACTCAGTCAGCCCCCGCCAAACGGCCTACAAAAAGAAGTTGGGAAAGAGTGAGTT	7260
Query	7261	TTCGTGCAGCATGAGCTACACCTGGACCGACGTGATTAGCTTCAAACCTGCTTCTAAAGT	7320
Sbjct	7261	TTCGTGCAGCATGAGCTACACTTGGACCGACGTGATTAGCTTCAAACCTGCTTCTAAAGT	7320
Query	7321	TCTGTCTGCAACTCGGGCCATCACTAGTGGTTTCCTCAAACAAAGATCATTGGTGTATGT	7380

Sbjct	7321	TCTGTCTGCAACTCGGGCCATCACTAGTGGTTTCCTCAAACAAAGATCATTGGTGTATGT	7380
Query	7381	GACTGAGCCGCGGGATGCGGAGCTTAGAAAACAAAAGTCACTATTAATAGACAACCTCT	7440
Sbjct	7381	GACTGAGCCGCGGGATGCGGAGCTTAGAAAACAAAAGTCACTATTAATAGACAACCTCT	7440
Query	7441	GTTCCCCCATCATACCACAAGCAAGTGAGATTGGCTAAGGAAAAAGCTTCAAAAGTTGT	7500
Sbjct	7441	GTTCCCCCATCATACCACAAGCAAGTGAGATTGGCTAAGGAAAAAGCTTCAAAAGTTGT	7500
Query	7501	CGGTGTCATGTGGGACTATGATGAAGTAGCAGCTCACACGCCCTCTAAGTCTGCTAAGTC	7560
Sbjct	7501	CGGTGTCATGTGGGACTATGATGAAGTAGCAGCTCACACGCCCTCTAAGTCTGCTAAGTC	7560
Query	7561	CCACATCACTGGCCTTCGGGGCACTGATGTTTCGTTCTGGAGCAGCCCGCAAGGCTGTTCT	7620
Sbjct	7561	CCACATCACTGGCCTTCGGGGCACTGATGTTTCGTTCTGGAGCAGCCCGCAAGGCTGTTCT	7620
Query	7621	GGACTTGCAGAAGTGTGTCGAGGCAGGTGAGATACCGAGTCATTATCGGCAAACCTGTGAT	7680
Sbjct	7621	GGACTTGCAGAAGTGTGTCGAGGCAGGTGAGATACCGAGTCATTATCGGCAAACCTGTGAT	7680
Query	7681	AGTTCCAAAGGAGGAGGTCTTCGTGAAGACCCCCAGAAACCAACAAAGAAACCCCCAAG	7740
Sbjct	7681	AGTTCCAAAGGAGGAGGTCTTCGTGAAGACCCCCAGAAACCAACAAAGAAACCCCCAAG	7740
Query	7741	GCTTATCTCGTACCCCCACCTTGAAATGAGATGTGTTGAGAAGATGTACTACGGTCAGGT	7800
Sbjct	7741	GCTTATCTCGTACCCCCACCTTGAAATGAGATGTGTTGAGAAGATGTACTACGGTCAGGT	7800
Query	7801	TGCTCCTGACGTAGTTAAAGCTGTCATGGGAGATGCGTACGGGTTTGTAGATCCACGTAC	7860
Sbjct	7801	TGCTCCTGACGTAGTTAAAGCTGTCATGGGAGATGCGTACGGGTTTGTGCGACCCACGTAC	7860
Query	7861	CCGTGTCAAGCGTCTGTTGTCGATGTGGTCACCCGATGCAGTCGGAGCCACATGCGATAC	7920
Sbjct	7861	CCGTGTCAAGCGTCTGTTGTCGATGTGGTCACCCGATGCAGTCGGAGCCACATGCGATAC	7920
Query	7921	AGTGTGTTTTGACAGTACCATCACACCCGAGGATATCATGGTGGAGACAGACATCTACTC	7980
Sbjct	7921	AGTGTGTTTTGACAGTACCATCACACCCGAGGATATCATGGTGGAGACAGACATCTACTC	7980
Query	7981	AGCAGCTAAACTCAGTGACCAACACCGAGCTGGCATTACACCATTGCGAGGCAGTTATA	8040
Sbjct	7981	AGCAGCTAAACTCAGTGACCAACACCGAGCTGGCATTACACCATTGCGAGGCAGTTATA	8040
Query	8041	CGCTGGAGGACCGATGATCGCTTATGATGGCCGAGAGATCGGATATCGTAGGTGTAGGTC	8100
Sbjct	8041	CGCTGGAGGACCGATGATCGCTTATGATGGCCGAGAGATCGGATATCGTAGGTGTAGGTC	8100
Query	8101	TTCCGGCGTCTATACTACCTCAAGTTCCAACAGTTTGACCTGCTGGCTGAAGGTAAATGC	8160
Sbjct	8101	TTCCGGCGTCTATACTACCTCAAGTTCCAACAGTTTGACCTGCTGGCTGAAGGTAAATGC	8160
Query	8161	TGCAGCCGAACAGGCTGGCATGAAGAACCCTCGCTTCCTTATTTGCGGCGATGATTGCAC	8220
Sbjct	8161	TGCAGCCGAACAGGCTGGCATGAAGAACCCTCGCTTCCTTATTTGCGGCGATGATTGCAC	8220
Query	8221	CGTAATTTGGAAGAGCGCCGGAGCAGATGCAGACAAACAAGCAATGCGTGTCTTTGCTAG	8280

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Sbjct 8221 CGTAATTTGGAAGAGCGCCGGAGCAGATGCAGACAAACAAGCAATGCGTGTCTTTGCTAG 8280
Query 8281 CTGGATGAAGGTGATGGGTGCACCACAAGATTGTGTGCCTCAACCCAAATACAGTTTGGA 8340
|||||
Sbjct 8281 CTGGATGAAGGTGATGGGTGCACCACAAGATTGTGTGCCTCAACCCAAATACAGTTTGGA 8340
Query 8341 AGAATTAACATCATGCTCATCAAATGTTACCTCTGGAATTACCAAAAGTGGCAAGCCTTA 8400
|||||
Sbjct 8341 AGAATTAACATCATGCTCATCAAATGTTACCTCTGGAATTACCAAAAGTGGCAAGCCTTA 8400
Query 8401 CTACTTTCTTACAAGAGATCCTCGTATCCCCCTTGGCAGGTGCTCTGCCGAGGGTCTGGG 8460
|||||
Sbjct 8401 CTACTTTCTTACAAGAGATCCTCGTATCCCCCTTGGCAGGTGCTCTGCCGAGGGTCTGGG 8460
Query 8461 ATACAACCCCAGTGCTGCGTGGATTGGGTATCTAATACATCACTACCCATGTTTGTGGGT 8520
|||||
Sbjct 8461 ATACAACCCCAGTGCTGCGTGGATTGGGTATCTAATACATCACTACCCATGTTTGTGGGT 8520
Query 8521 TAGCCGTGTGTTGGCTGTCCATTTTCATGGAGCAGATGCTCTTTGAGGACAAACTTCCCGA 8580
|||||
Sbjct 8521 TAGCCGTGTGTTGGCTGTCCATTTTCATGGAGCAGATGCTCTTTGAGGACAAACTTCCCGA 8580
Query 8581 GACGGTGACCTTTGACTGGTATGGGAAAAATTATACGGTGCCTGTAGAAGATCTGCCAG 8640
|||
Sbjct 8581 GACTGTGACCTTTGACTGGTATGGGAAAAATTATACGGTGCCTGTAGAAGATCTGCCAG 8640
Query 8641 CATCATTGCTGGTGTGCACGGTATTGAGGCTTTCTCGGTGGTGCCTACACCAACGCTGA 8700
|||||
Sbjct 8641 CATCATTGCTGGTGTGCACGGTATTGAGGCTTTCTCGGTGGTGCCTACACCAACGCTGA 8700
Query 8701 GATCCTCAGAGTTTCCCAATCACTAACAGACATGACCATGCCCCCCTGCGAGCCTGGCG 8760
|||||
Sbjct 8701 GATCCTCAGAGTTTCCCAATCACTAACAGACATGACCATGCCCCCCTGCGAGCCTGGCG 8760
Query 8761 AAAGAAAGCCAGGGCGGTCTCGCCAGCGCCAAGAGGCGTGGCGGAGCACACGCAAAATT 8820
|||||
Sbjct 8761 AAAGAAAGCCAGGGCGGTCTCGCCAGCGCCAAGAGGCGTGGCGGAGCACACGCAAAATT 8820
Query 8821 GGCTCGCTTCCTTCTCTGGCATGCTACATCTAGACCTCTACCAGATTTGGATAAGACGAG 8880
|||||
Sbjct 8821 GGCTCGCTTCCTTCTCTGGCATGCTACATCTAGACCTCTACCAGATTTGGATAAGACGAG 8880
Query 8881 CGTGGCTCGGTACACCACTTTCAATTATTGTGATGTTTACTCCCCGAGGGGGATGTGTT 8940
|||||
Sbjct 8881 CGTGGCTCGGTACACCACTTTCAATTATTGTGATGTTTACTCCCCGAGGGGGATGTGTT 8940
Query 8941 TATTACACCACAGAGAAGATTGCAGAAGTTTCTTGTGAAGTATTTGGCTGTCATTGTTTT 9000
|
Sbjct 8941 TGTTACACCACAGAGAAGATTGCAGAAGTTTCTTGTGAAGTATTTGGCTGTCATTGTTTT 9000
Query 9001 TGCCCTAGGGCTCATTGCTGTTGGATTAGCCATCAGCTGAACCCCCAAATTCAAATTA 9060
|||||
Sbjct 9001 TGCCCTAGGGCTCATTGCTGTTGGACTAGCCATCAGCTGAACCCCCAAATTCAAATTA 9060
Query 9061 CTAACAG----TTTTTTTTTTTTTTTTTTTTTTTTTTAGGGCAGCGGCAACAGGGGAGACCCC 9116
|||||
Sbjct 9061 TTAACAGTTTTTTTTTTTTTTTTTTTTTTTTTTAGGGCAGCGGCAACAGGGGAGACCCC 9120
Query 9117 GGGCTTAACGACCCCGC 9133
|||||
```

Sbjct 9121 GGGCTTAACGACCCCGC 9137

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 1

Number of Hits to DB: 4623

Number of extensions: 84

Number of successful extensions: 19

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 9399

Length of database: 19,583,881,279

Length adjustment: 28

Effective length of query: 9371

Effective length of database: 19,583,881,251

Effective search space: 183520551203121

Effective search space used: 183520551203121

X1: 11 (21.1 bits)

X2: 26 (50.0 bits)

X3: 26 (50.0 bits)

S1: 16 (31.5 bits)

S2: 23 (44.9 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.15 [Oct-15-2006]

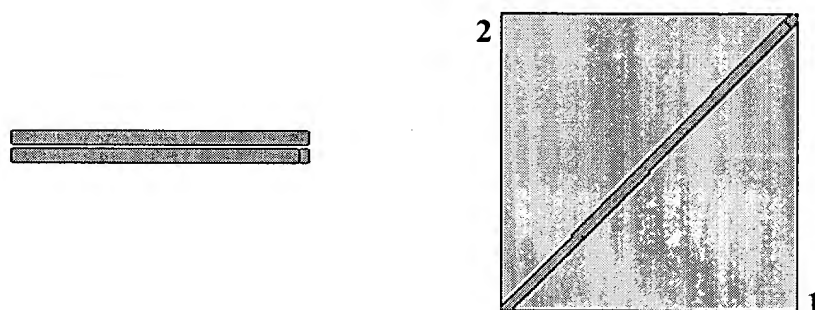
Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☐ View option
 Masking character option Masking color option
☐ Show CDS translation

Sequence 1: lcl|seq_1

Length = 9399 (1 .. 9399)

Sequence 2: gi|13162187|emb|AJ277947.1|Hepatitis GB virus B genomic RNA

Length = 9397 (1 .. 9397)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.



Score = 1.785e+04 bits (9283), Expect = 0.0
 Identities = 9362/9399 (99%), Gaps = 2/9399 (0%)
 Strand=Plus/Plus

Query	1	ACCACAAACACTCCAGTTTGTACACTCCGCTAGGAATGCTCCTGGAGCACCCCCCTAG	60
Sbjct	1	ACCACAAACACTCCAGTTTGTACACTCCGCTAGGAATGCTCCTGGAGCACCCCCCTAG	60
Query	61	CAGGGCGTGGGGGATTTCCTGCCCCTGCTGCAGAAGGGTGGAGCCAACCACCTTAGTAT	120
Sbjct	61	CAGGGCGTGGGGGATTTCCTGCCCCTGCTGCAGAAGGGTGGAGCCAACCACCTTAGTAT	120
Query	121	GTAGGCGGCGGGACTCATGACGCTCGCGTGATGACAAGCGCCAAGCTTGACTTGGATGGC	180

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Sbjct 121 GTAGGCGGCGGGACTCATGACGCTCGCGTGATGACAAGCGCCAAGCTTGACTTGGATGGC 180
Query 181 CCTGATGGGCGTTTCATGGGTTTCGGTGGTGGTGGCGCTTTAGGCAGCCTCCACGCCCACCA 240
|||||
Sbjct 181 CCTGATGGGCGTTTCATGGGTTTCGGTGGTGGTGGCGCTTTAGGCAGCCTCCACGCCCACCA 240
Query 241 CCTCCCAGATAGAGCGGCGGCACTGTAGGGAAGACCGGGGACCGGTCACTACCAAGGACG 300
|||||
Sbjct 241 CCTCCCAGATAGAGCGGCGGCACTGTAGGGAAGACCGGGGACCGGTCACTACCAAGGACG 300
Query 301 CAGACCTCTTTTTGAGTATCACGCCTCCGGAAGTAGTTGGGCAAGCCCACCTATATGTGT 360
|||||
Sbjct 301 CAGACCTCTTTTTGAGTATCACGCCTCCGGAAGTAGTTGGGCAAGCCCACCTATATGTGT 360
Query 361 TGGGATGGTTGGGGTTAGCCATCCATACCGTACTGCCTGATAGGGTCCTTGCGAGGGGAT 420
|||||
Sbjct 361 TGGGATGGTTGGGGTTAGCCATCCATACCGTACTGCCTGATAGGGTCCTTGCGAGGGGAT 420
Query 421 CTGGGAGTCTCGTAGACCGTAGCACATGCCTGTTATTTCTACTCAAACAAGTCCTGTACC 480
|||||
Sbjct 421 CTGGGAGTCTCGTAGACCGTAGCACATGCCTGTTATTTCTACTCAAACAAGTCCTGTACC 480
Query 481 TGCGCCCAAGACGCGCAAGAACAAGCAGACGCAGGCTTCATATCCTGTGTCCATTAAAAC 540
|||||
Sbjct 481 TGCGCCCAAGACGCGCAAGAACAAGCAGACGCAGGCTTCATATCCTGTGTCCATTAAAAC 540
Query 541 ATCTGTTGAAAGGGGACAACGAGCAAAGCGCAAAGTCCAGCGCGATGCTCGGCCTCGTAA 600
|||||
Sbjct 541 ATCTGTTGAAAGGGGACAACGAGCAAAGCGCAAAGTCCAGCGCGATGCTCGGCCTCGTAA 600
Query 601 TTACAAAATTGCTGGTATCCATGATGGCTTGCAGACATTGGCTCAGGCTGCTTTGCCAGC 660
|||||
Sbjct 601 TTACAAAATTGCTGGTATCCATGATGGCTTGCAGACATTGGCTCAGGCTGCTTTGCCAGC 660
Query 661 TCATGGTTGGGGACGCCAAGACCCTCGCCATAAGTCTCGCAATCTTGGAATCCTTCTGGA 720
|||||
Sbjct 661 TCATGGTTGGGGACGCCAAGACCCTCGCCATAAGTCTCGCAATCTTGGAATCCTTCTGGA 720
Query 721 TTACCCTTTGGGGTGGATTGGTGTATGTTACAACCTCACACACCTCTAGTAGGCCCGCTGGT 780
|||||
Sbjct 721 TTACCCTTTGGGGTGGATTGGTGTATGTTACAACCTCACACACCTCTAGTAGGCCCGCTGGT 780
Query 781 GGCAGGAGCGGTCGTTTCGACCAGTCTGCCAGATAGTACGCTTGCTGGAGGATGGAGTCAA 840
|||||
Sbjct 781 GGCAGGAGCGGTCGTTTCGACCAGTCTGCCAGATAGTACGCTTGCTGGAGGATGGAGTCAA 840
Query 841 CTGGGCTACTGGTTGGTTCGGTGTCCACCTTTTTGTGGTATGTCTGCTATCTTTGGCCTG 900
|||||
Sbjct 841 CTGGGCTACTGGTTGGTTCGGTGTCCACCTTTTTGTGGTATGTCTGCTATCTTTGGCCTG 900
Query 901 TCCCTGTAGTGGGGCGCGGGTCACTGACCCAGACACAAATACCACAATCCTGACCAATTG 960
|||||
Sbjct 901 TCCCTGTAGTGGGGCGCGGGTCACTGACCCAGACACAAATACCACAATCCTGACCAATTG 960
Query 961 CTGCCAGCGTAATCAGGTTATCTATTGTTCTCCTTCCACTTGCTACACGAGCCTGGTTG 1020
|||||
Sbjct 961 CTGCCAGCGTAATCAGGTTATCTATTGTTCTCCTTCCACTTGCTACACGAGCCTGGTTG 1020
Query 1021 TGTGATCTGTGCGGACGAGTGCTGGGTTCCCGCCAATCCGTACATCTCACACCCTTCCAA 1080
|||||
```

Sbjct	1021	TGTGATCTGTGCGGACGAGTGCTGGGTTCCCGCCAATCCGTACATCTCACACCCTTCCAA	1080
Query	1081	TTGGACTGGCACGGACTCCTTCTTGGCTGACCACATTGATTTTGTATGGGCGCTCTTGT	1140
Sbjct	1081	TTGGACTGGCACGGACTCCTTCTTGGCTGACCACATTGATTTTGTATGGGCGCTCTTGT	1140
Query	1141	GACCTGTGACGCCCTTGACATTGGTGAGTTGTGTGGTGCGTGTGTATTAGTCGGTGACTG	1200
Sbjct	1141	GACCTGTGACGCCCTTGACATTGGTGAGTTGTGTGGTGCGTGTGTATTAGTCGGTGACTG	1200
Query	1201	GCTTGTGAGGCACTGGCTTATTACATAGACCTCAATGAACTGGTACTTGTTACCTGGA	1260
Sbjct	1201	GCTTGTGAGGCACTGGCTTATTACATAGACCTCAATGAACTGGTACTTGTTACCTGGA	1260
Query	1261	AGTGCCCACTGGAATAGATCCTGGGTTTCTAGGGTTTATCGGGTGGATGGCCGGCAAGGT	1320
Sbjct	1261	AGTGCCCACTGGAATAGATCCTGGGTTTCTAGGGTTTATCGGGTGGATGGCCGGCAAGGT	1320
Query	1321	CGAGGCTGTCATCTTCTTGACCAAAGTGGCTTCACAAGTACCATACGCTATTGCGACTAT	1380
Sbjct	1321	CGAGGCTGTCATCTTCTTGACCAAAGTGGCTTCACAAGTACCATACGCTATTGCGACTAT	1380
Query	1381	GTTTAGCAGTGTACACTACCTGGCGGTTGGCGCTCTGATCTACTATGCCTCTCGGGGCAA	1440
Sbjct	1381	GTTTAGCAGTGTACACTACCTGGCGGTTGGCGCTCTGATCTACTATGCCTCTCGGGGCAA	1440
Query	1441	GTGGTATCAGTTGCTCCTAGCGCTTATGCTTTACATAGAAGCGACCTCTGGAAACCCTAT	1500
Sbjct	1441	GTGGTATCAGTTGCTCCTAGCGCTTATGCTTTACATAGAAGCGACCTCTGGAAACCCCAT	1500
Query	1501	CAGGGTGCCCACTGGATGCTCAATAGCTGAGTTTTGCTCGCCTTTGATGATACCATGTCC	1560
Sbjct	1501	CAGGGTGCCCACTGGATGCTCAATAGCTGAGTTTTGCTCGCCTTTGATGATACCATGTCC	1560
Query	1561	TTGCCACTCTTATTTGAGTGAGAATGTGTCAGAAGTCATTTGTTACAGTCCAAAGTGGAC	1620
Sbjct	1561	TTGCCACTCTTATTTGAGTGAGAATGTGTCAGAAGTCATTTGTTACAGTCCAAAGTGGAC	1620
Query	1621	CAGGCCTATCACTCTAGAGTATAACAACCTCCATATCTTGGTACCCCTATACAATCCCTGG	1680
Sbjct	1621	CAGGCCTGTCACCTCTAGAGTATAACAACCTCCATATCTTGGTACCCCTATACAATCCCTGG	1680
Query	1681	TGCGAGGGGATGTATGGTTAAATTCAAAAATAACACATGGGGTTGCTGCCGTATTGCGAA	1740
Sbjct	1681	TGCGAGGGGATGTATGGTTAAATTCAAAAATAACACATGGGGTTGTTGCCGTATTGCGAA	1740
Query	1741	TGTGCCATCGTACTGCACTATGGGCACTGATGCAGTGTGGAACGACACTCGCAACACTTA	1800
Sbjct	1741	TGTGCCATCGTACTGCACTATGGGCACTGATGCAGTGTGGAACGACACTCGCAACACTTA	1800
Query	1801	CGAAGTATGCGGTGTAACACCATGGCTAACAACCGCATGGCACAACGGCTCAGCCCTGAA	1860
Sbjct	1801	CGAAGCATGCGGTGTAACACCATGGCTAACAACCGCATGGCACAACGGCTCAGCCCTGAA	1860
Query	1861	ATTGGCTATATTACAATACCCTGGGTCTAAAGAAATGTTTAAACCTCATAATTGGATGTC	1920
Sbjct	1861	ATTGGCTATATTACAATACCCTGGGTCTAAAGAAATGTTTAAACCTCATAATTGGATGTC	1920
Query	1921	AGGCCATTTGTATTTTGGGGATCAGATACCCCTATAGTTTACTTTTATGACCCTGTGAA	1980

Sbjct	1921	AGGCCATTTGTATTTTGAGGGATCAGATACCCCTATAGTTTACTTTTATGACCCTGTGAA	1980
Query	1981	TTCCACTCTCCTACCACCGGAGAGGTGGGCTAGGTTGCCCCGTACCCACCTGTGGTACG	2040
Sbjct	1981	TTCCACTCTCCTACCACCGGAGAGGTGGGCTAGGTTGCCCCGTACCCACCTGTGGTACG	2040
Query	2041	TGGTTCTTGGTTACAGGTTCCGCAAGGGTTTTACAGTGATGTGAAAGACCTAGCCACAGG	2100
Sbjct	2041	TGGTTCTTGGTTACAGGTTCCGCAAGGGTTTTACAGTGATGTGAAAGACCTAGCCACAGG	2100
Query	2101	ATTGATCACCAAAGACAAAGCCTGGAAAAATTATCAGGTCTTATATTCCGCCACGGGTGC	2160
Sbjct	2101	ATTGATCACCAAAGACAAAGCCTGGAAAAATTATCAGGTCTTATATTCCGCCACGGGTGC	2160
Query	2161	TTTGTCTCTTACGGGAGTTACCACCAAGGCCGTGGTGCTAATTCTGTTGGGGTTGTGTGG	2220
Sbjct	2161	TTTGTCTCTTACGGGAGTTACCACCAAGGCCGTGGTGCTAATTCTGTTGGGGTTGTGTGG	2220
Query	2221	CAGCAAGTATCTTATTTTAGCCTACCTCTGTTACTTGTCCCTTTGTTTTGGGCGCGCTTC	2280
Sbjct	2221	CAGCAAGTATCTTATTTTAGCCTACCTCTGTTACTTGTCCCTTTGTTTTGGGCGCGCTTC	2280
Query	2281	TGGTTACCCTTTGCGTCCTGTGCTCCCATCCCAGTCGTATCTCCAAGCTGGCTGGGATGT	2340
Sbjct	2281	TGGTTACCCTTTGCGTCCTGTGCTCCCATCCCAGTCGTATCTCCAAGCTGGCTGGGATGT	2340
Query	2341	TTTGTCTAAAGCTCAAGTAGCTCCTTTTGCTTTGATTTTCTTCATCTGTTGCTATCTCCG	2400
Sbjct	2341	TTTGTCTAAAGCTCAAGTAGCTCCTTTTGCTTTGATTTTCTTCATCTGTTGCTATCTCCG	2400
Query	2401	CTGCAGGCTACGTTATGCTGCCCTTTTAGGGTTTGTGCCCATGGCTGCGGGCTTGCCCCCT	2460
Sbjct	2401	CTGCAGGCTACGTTATGCTGCCCTTTTAGGGTTTGTGCCCATGGCTGCGGGCTTGCCCCCT	2460
Query	2461	AACTTTCTTTGTTGCAGCAGCTGCTGCCCAACCAGATTATGACTGGTGGGTGCGACTGCT	2520
Sbjct	2461	AACTTTCTTTGTTGCAGCAGCTGCTGCCCAACCAGATTATGACTGGTGGGTGCGACTGCT	2520
Query	2521	AGTGGCAGGGTTAGTTTTGTGGGCCGGCCGTAACCGTGGTCACCGCATAGCTCTGCTTGT	2580
Sbjct	2521	AGTGGCAGGGTTAGTTTTGTGGGCCGGCCGTAACCGTGGTCACCGCATAGCTCTGCTTGT	2580
Query	2581	AGGTCCTTGGCCTCTGGTAGCGCTTTTAACCCTCTTGCATTTGGTTACGCCTGCTTCAGC	2640
Sbjct	2581	AGGTCCTTGGCCTCTGGTAGCGCTTTTAACCCTCTTGCATTTGGTTACGCCTGCTTCAGC	2640
Query	2641	TTTTGATACCGAGATAATTGGAGGGCTGACAATACCACCTGTAGTAGCATTAGTTGTCAT	2700
Sbjct	2641	TTTTGATACCGAGATAATTGGAGGGCTGACAATACCACCTGTAGTAGCATTAGTTGTCAT	2700
Query	2701	GTCTCGTTTTGGCTTCTTTGCTCACTTGTTACCTCGCTGTGCTTTAGTTAACTCCTATCT	2760
Sbjct	2701	GTCTCGTTTTGGCTTCTTTGCTCACTTGTTACCTCGCTGTGCTTTAGTTAACTCCTATCT	2760
Query	2761	TTGGCAACGTTGGGAGAATTGGTTTTGGAACGTTACACTAAGACCGGAGAGGTTTTTCCT	2820
Sbjct	2761	TTGGCAACGTTGGGAGAATTGGTTTTGGAACGTTACACTAAGACCGGAGAGGTTTTTCCT	2820
Query	2821	TGTGCTGGTTTTGTTTCCCCGGTGCGACATATGACGCGCTGGTGACTTTCTGTGTGTGTCA	2880

Sbjct	2821	TGTGCTGGTTTGTTCCTCCCGGTGCGACATATGACGCGCTGGTGACTTTCTGTGTGTGTCA	2880
Query	2881	CGTAGCTCTTCTATGTTTAAACATCCAGTGCAGCATCGTTCTTTGGGACTGACTCTAGGGT	2940
Sbjct	2881	CGTAGCTCTCCTATGTTTAAACATCCAGTGCAGCATCGTTCTTTGGGACTGACTCTAGGGT	2940
Query	2941	TAGGGCCCATAGAATGTTGGTGCGTCTCGGAAAGTGTCATGCTTGGTATTCTCATTATGT	3000
Sbjct	2941	TAGGGCCCATAGAATGTTGGTGCGTCTCGGAAAGTGCCATGCTTGGTATTCTCATTATGT	3000
Query	3001	TCTTAAGTTTTTCTCTTAGTGTTTGGTGAGAATGGTGTGTTTTTCTATAAGCACTTGCA	3060
Sbjct	3001	TCTTAAGTTTTTCTCTTAGTGTTTGGTGAGAATGGTGTGTTTTTCTATAAGCACTTGCA	3060
Query	3061	TGGTGATGTCTTGCCTAATGATTTTGCCTCGAACTACCATTGCAAGAGCCATTTTTCCC	3120
Sbjct	3061	TGGTGATGTCTTGCCTAATGATTTTGCCTCGAACTACCATTGCAAGAGCCATTTTTCCC	3120
Query	3121	TTTTGAAGGCAAGGCAAGGGTCTATAGGAATGAAGGAAGACGCTTGGCGTGTGGGGACAC	3180
Sbjct	3121	TTTTGAAGGCAAGGCAAGGGTCTATAGGAATGAAGGAAGACGCTTGGCGTGTGGGGACAC	3180
Query	3181	GGTTGATGGTTTGGCCGTTGTTGCGCGTCTCGGCGACCTTGTTTTCGCAGGGTTGGCTAT	3240
Sbjct	3181	GGTTGATGGTTTGGCCGTTGTTGCGCGTCTCGGCGACCTTGTTTTCGCAGGGTTAGCTAT	3240
Query	3241	GCCGCCAGATGGGTGGGCCATTACCGCACCTTTTACGCTGCAGTGTCTCTCTGAACGTGG	3300
Sbjct	3241	GCCGCCAGATGGGTGGGCCATTACCGCACCTTTTACGCTGCAGTGTCTCTCTGAACGTGG	3300
Query	3301	CACGCTGTCTAGCGATGGCAGTGGTCATGACTGGTATAGACCCCGAACTTGGACTGGAAC	3360
Sbjct	3301	CACGCTGTCTAGCGATGGCAGTGGTCATGACTGGTATAGACCCCGAACTTGGACTGGAAC	3360
Query	3361	TATCTTCAGATTAGGATCTCTGGCCACTAGCTACATGGGATTTGTTTGTGACAACGTGTT	3420
Sbjct	3361	TATCTTCAGATTAGGATCTCTGGCCACTAGCTACATGGGATTTGTTTGTGACAACGTGTT	3420
Query	3421	GTATACTGCTCACCATGGCAGCAAGGGGCGCCGGTTGGCTCATCCCACAGGCTCTATACA	3480
Sbjct	3421	GTATACTGCTCACCATGGCAGCAAGGGGCGCCGGTTGGCTCATCCCACAGGCTCCATACA	3480
Query	3481	CCCAATAACCGTTGACGCGGCTAATGACCAGGACATCTATCAACCACCATGTGGAGCTGG	3540
Sbjct	3481	CCCAATAACCGTTGACGCGGCTAATGACCAGGACATCTATCAACCACCATGTGGAGCTGG	3540
Query	3541	GTCCCTTACTCGGTGCTCTTGCGGGGAGACCAAGGGGTATCTGGTAACACGACTGGGGTC	3600
Sbjct	3541	GTCCCTTACTCGGTGCTCTTGCGGGGAGACCAAGGGGTATCTGGTAACACGACTGGGGTC	3600
Query	3601	ATTGGTTGAGGTCAACAAATCCGATGACCCTTATTGGTGTGTGTGCGGGGCCCTTCCCAT	3660
Sbjct	3601	ATTGGTTGAGGTCAATAAATCCGATGACCCTTATTGGTGTGTGTGCGGGGCCCTTCCCAT	3660
Query	3661	GGCTGTTGCCAAGGGTTCTTCAGGTGCCCCGATTCTGTGCTCCTCCGGGCATGTTATTGG	3720
Sbjct	3661	GGCTGTTGCCAAGGGTTCTTCAGGTGCCCCGATTCTGTGCTCCTCCGGGCATGTTATTGG	3720
Query	3721	GATGTTACCGCTGCTAGAAATTCTGGCGGTTGAGTCAGTCAGATTAGGGTTAGGCCGTT	3780

Sbjct	3721	GATGTTACCGCTGCTAGAAATTCTGGCGGTTCAAGTCAGCCAGATTAGGGTTAGGCCGTT	3780
Query	3781	GGTGTGTGCTGGATACCATCCCCAGTACACAGCAQATGCCACTCTTGATACAAAACCTAC	3840
Sbjct	3781	GGTGTGTGCTGGATACCATCCCCAGTACACAGCACATGCCACTCTTGATACAAAACCTAC	3840
Query	3841	TGTGCCTAACGAGTATTCAAGTGCAAATTTTAATTGCCCCCACTGGCAGCGGCAAGTCAAC	3900
Sbjct	3841	TGTGCCTAACGAGTATTCAAGTGCAAATTTTAATTGCCCCCACTGGCAGCGGCAAGTCAAC	3900
Query	3901	CAAATTACCACTTTCTTACATGCAGGAGAAGTATGAGGTCTTGGTCCTAAATCCCAGTGT	3960
Sbjct	3901	CAAATTACCACTTTCTTACATGCAGGAGAAGTATGAGGTCTTGGTCCTAAATCCCAGTGT	3960
Query	3961	GGCTACAACAGCATCAATGCCAAAGTACATGCACGCGACGTACGGCGTGAATCCAAATTG	4020
Sbjct	3961	GGCTACAACAGCATCAATGCCAAAGTACATGCACGCGACGTACGGCGTGAATCCAAATTG	4020
Query	4021	CTATTTTAATGGCAAATGTACCAACACAGGGGCTTCACTTACGTACAGCACATATGGCAT	4080
Sbjct	4021	CTATTTTAATGGCAAATGTACCAACACAGGGGCTTCACTTACGTACAGCACATATGGCAT	4080
Query	4081	GTACCTGACCGGAGCATGTTCCCGGAACATGATGTAATCATTGTGACGAATGCCATGC	4140
Sbjct	4081	GTACCTGACCGGAGCATGTTCCCGGAACATGATGTAATCATTGTGACGAATGCCATGC	4140
Query	4141	TACCGATGCAACCACCGTGTTGGGCATTGGAAAGGTCTAACCGAAGCTCCATCCAAAAA	4200
Sbjct	4141	TACCGATGCAACCACCGTGTTGGGCATTGGAAAGGTCTAACCGAAGCTCCATCCAAAAA	4200
Query	4201	TGTTAGGCTAGTGGTTCTTGCCACGGCTACCCCCCTGGAGTAATCCCTACACCACATGC	4260
Sbjct	4201	TGTTAGGCTAGTGGTTCTTGCCACGGCTACCCCCCTGGAGTAATCCCTACACCACATGC	4260
Query	4261	CAACATAACTGAGATTCAATTAACCGATGAAGGCACTATCCCCTTTTCATGGAAAAAAGAT	4320
Sbjct	4261	CAACATAACTGAGATTCAATTAACCGATGAAGGCACTATCCCCTTTTCATGGAAAAAAGAT	4320
Query	4321	TAAGGAGGAAAATCTGAAGAAAGGGAGACACCTTATCTTTGAGGCTACCAAAAAACACTG	4380
Sbjct	4321	TAAGGAGGAAAATCTGAAGAAAGGGAGACACCTTATCTTTGAGGCTACCAAAAAACACTG	4380
Query	4381	TGATGAGCTTGCTAACGAGTTAGCTCGAAAGGGAATAACAGCTGTCTCTTACTATAGGGG	4440
Sbjct	4381	TGATGAGCTTGCTAACGAGTTAGCTCGAAAGGGAATAACAGCTGTCTCTTACTATAGGGG	4440
Query	4441	ATGTGACATCTCAAAAATCCCTGAGGGCGACTGTGTAGTAGTTGCCACTGATGCCTTGTG	4500
Sbjct	4441	ATGTGACATCTCAAAAATCCCTGAGGGCGACTGTGTAGTAGTTGCCACTGATGCCTTGTG	4500
Query	4501	TACAGGGTACACTGGTGACTTTGATTCCGTGTATGACTGCAGCCTCATGGTAGAAGGCAC	4560
Sbjct	4501	TACAGGGTACACTGGTGACTTTGATTCCGTGTATGACTGCAGCCTCATGGTAGAAGGCAC	4560
Query	4561	ATGCCATGTTGACCTTGACCCTACTTTCACCATGGGTGTTTCGTGTGTGCGGGGTTTCAGC	4620
Sbjct	4561	ATGCCATGTTGACCTTGACCCTACTTTCACCATGGGTGTTTCGTGTGTGCGGGGTTTCAGC	4620
Query	4621	AATAGTTAAAGGCCAGCGTAGGGGCCGCACAGGCCGTGGGAGAGCTGGCATATACTACTA	4680

Sbjct	4621	AATAGTTAAAGGCCAGCGTAGGGGCCGCACAGGCCGTGGGAGAGCTGGCATATACTACTA	4680
Query	4681	TGTAGACGGGAGTTGTACCCCTTCGGGTATGGTTCCTGAATGCAACATTGTTGAAGCCTT	4740
Sbjct	4681	TGTAGACGGGAGTTGTACCCCTTCGGGTATGGTTCCTGAATGCAACATTGTTGAAGCCTT	4740
Query	4741	CGACGCAGCCAAGGCATGGTATGGTTTGTTCATCAACAGAAGCTCAAACCTATTCTGGACAC	4800
Sbjct	4741	CGACGCAGCCAAGGCATGGTATGGTTTGTTCATCAACAGAAGCTCAAACCTATTCTGGACAC	4800
Query	4801	CTATCGCACCCAACCTGGGTACCTGCGATAGGAGCAAATTTGGACGAGTGGGCTGATCT	4860
Sbjct	4801	CTATCGCACCCAACCTGGGTACCTGCGATAGGAGCAAATTTGGACGAGTGGGCTGATCT	4860
Query	4861	CTTTTCTATGGTCAACCCCGAACCTTCATTTGTCAATACTGCAAAAAGAACTGCTGACAA	4920
Sbjct	4861	CTTTTCAATGGTCAACCCCGAACCTTCATTTGTCAATACTGCAAAAAGAACTGCTGACAA	4920
Query	4921	TTATGTTTTGTTGACTGCAGCCCAACTACAACGTGTGCATCAGTATGGCTATGCTGCTCC	4980
Sbjct	4921	TTATGTTTTGTTGACTGCAGCCCAACTACAACGTGTGCATCAGTATGGCTATGCTGCTCC	4980
Query	4981	CAATGACGCACCACGGTGGCAGGGAGCCCGGCTTGGGAAAAACCTTGTGGGGTTCTGTG	5040
Sbjct	4981	CAATGACGCACCACGGTGGCAGGGAGCCCGGCTTGGGAAAAACCTTGTGGGGTTCTGTG	5040
Query	5041	GCGCTTGGACGGCGCTGACGCCTGTCCTGGCCCAGAGCCCAGCGAGGTGACCAGATACCA	5100
Sbjct	5041	GCGCTTGGACGGCGCTGACGCCTGTCCTGGCCCAGAGCCCAGCGAGGTGACCAGATACCA	5100
Query	5101	AATGTGCTTCACTGAAGTCAATACTTCTGGGACAGCCGCACTCGCTGTTGGCGTTGGAGT	5160
Sbjct	5101	AATGTGCTTCACTGAAGTCAATACTTCTGGGACAGCCGCACTCGCTGTTGGCGTTGGAGT	5160
Query	5161	GGCTATGGCTTATCTAGCCATTGACACTTTTGGCGCCACTTGTGTGCGGCGTTGCTGGTC	5220
Sbjct	5161	GGCTATGGCTTATCTAGCCATTGACACTTTTGGCGCCACTTGTGTGCGGCGTTGCTGGTC	5220
Query	5221	TATTGCATCAGTCCCTACCGGTGCTACTGTCGCCCCAGTGGTTGACGAAGAAGAAATCGT	5280
Sbjct	5221	TATTACATCAGTCCCTACCGGTGCTACTGTCGCCCCAGTGGTTGACGAAGAAGAAATCGT	5280
Query	5281	GGAGGAGTGTGCATCATTCATTCCCTTGGAGGCCATGGTTGCTGCAATCGATAAGCTGAA	5340
Sbjct	5281	GGAGGAGTGTGCATCATTCATTCCCTTGGAGGCCATGGTTGCTGCAATTGACAAGCTGAA	5340
Query	5341	GAGTACAATCACCACAACCTAGTCCTTTTACATTGGAAACCGCCCTTGAAAACTTAACAC	5400
Sbjct	5341	GAGTACAATCACCACAACCTAGTCCTTTTACATTGGAAACCGCCCTTGAAAACTTAACAC	5400
Query	5401	CTTTCTTGGGCCTCATGCAGCTACAATCCTTGCTATCATAGAGTATTGCTGTGGTTAGT	5460
Sbjct	5401	CTTTCTTGGGCCTCATGCAGCTACAATCCTTGCTATCATAGAGTATTGCTGTGGCTTAGT	5460
Query	5461	CACCTTACCTGACAATCCCTTTGCATCATGCGTGTTTGCTTTTATTGCGGGTATTACTAC	5520
Sbjct	5461	CACCTTACCTGACAATCCCTTTGCATCATGCGTGTTTGCTTTTATTGCGGGTATTACTAC	5520
Query	5521	CCCACTACCTCACAAGATCAAAATGTTTCCTGTCAATTATTTGGAGGCGCAATTGCGTCCAA	5580

Sbjct	5521	CCCACTACCTCACAAGATCAAAATGTTCTGTCTATTATTTGGAGGCGCAATTGCGTCCAA	5580
Query	5581	GCTTACAGACGCTAGAGGCGCACTGGCGTTCATGATGGCCGGGGCTGCGGGAACAGCTCT	5640
Sbjct	5581	GCTTACAGACGCTAGAGGCGCACTGGCGTTCATGATGGCCGGGGCTGCGGGAACAGCTCT	5640
Query	5641	TGGTACATGGACATCGGTGGGTTTTGTCTTTGACATGCTAGGCGGCTATGCTGCCGCCTC	5700
Sbjct	5641	TGGTACATGGACATCGGTGGGTTTTGTCTTTGACATGCTAGGCGGCTATGCTGCCGCCTC	5700
Query	5701	ATCCACTGCTTGCTTGACATTTAAATGCTTGATGGGTGAGTGGCCCACTATGGATCAGCT	5760
Sbjct	5701	ATCCACTGCTTGCTTGACATTTAAATGCTTGATGGGTGAGTGGCCCACTATGGATCAGCT	5760
Query	5761	TGCTGGTTTAGTCTACTCCGCGTTCAATCCGGCCGCAGGAGTTGTGGGCGTCTTGTGAGC	5820
Sbjct	5761	TGCTGGTTTAGTCTACTCCGCGTTCAACCCGGCCGCAGGAGTTGTGGGCGTCTTGTGAGC	5820
Query	5821	TTGTGCAATGTTTGCTTTGACAACAGCAGGGCCAGATCACTGGCCCAACAGACTTCTTAC	5880
Sbjct	5821	TTGTGCAATGTTTGCTTTGACAACAGCAGGGCCAGATCACTGGCCCAACAGACTTCTTAC	5880
Query	5881	TATGCTTGCTAGGAGCAACACTGTATGTAATGAGTACTTTATTGCCACTCGTGACATCCG	5940
Sbjct	5881	TATGCTTGCTAGGAGCAACACTGTATGTAATGAGTACTTTATTGCCACTCGTGACATCCG	5940
Query	5941	CAGGAAGATACTGGGCATTCTGGAGGCATCTACCCCCTGGAGTGTGATATCAGCTTGCAT	6000
Sbjct	5941	CAGGAAGATACTGGGCATTCTGGAGGCATCTACCCCCTGGAGTGTGATATCAGCTTGCAT	6000
Query	6001	CCGTTGGCTCCACACCCCGACGGAGGATGATTGCGGCCTCATTGCTTGGGGTCTAGAGAT	6060
Sbjct	6001	CCGTTGGCTCCACACCCCGACGGAGGATGATTGCGGCCTCATTGCTTGGGGTCTAGAGAT	6060
Query	6061	TTGGCAGTATGTGTGCAATTTCTTTGTGATTGCTTTAATGTCCTTAAAGCTGGAGTTCA	6120
Sbjct	6061	TTGGCAGTACGTGTGCAATTTCTTTGTGATTGCTTTAATGTCCTTAAAGCTGGAGTTCA	6120
Query	6121	GAGCATGGTTAACATTCTGGTTGTCCTTTCTACAGCTGCCAGAAGGGGTACAAGGGCCC	6180
Sbjct	6121	GAGCATGGTTAACATTCTGGTTGTCCTTTCTACAGCTGCCAGAAGGGGTACAAGGGCCC	6180
Query	6181	CTGGATTGGATCAGGTATGCTCCAAGCACGCTGTCCATGCGGTGCTGAACCTCATCTTTTC	6240
Sbjct	6181	CTGGATTGGATCAGGTATGCTCCAAGCACGCTGTCCATGCGGTGCTGAACCTCATCTTTTC	6240
Query	6241	TGTTGAGAATGGTTTTGCAAAACTTTACAAAGGACCCAGAAGTGTTCAAATTACTGGAG	6300
Sbjct	6241	TGTTGAGAATGGTTTTGCAAAACTTTACAAAGGACCCAGAAGTGTTCAAATTACTGGAG	6300
Query	6301	AGGGGCTGTTCCAGTCAACGCTAGGCTGTGTGGGTGCGCTAGACCGGACCCAACTGATTG	6360
Sbjct	6301	AGGGGCTGTTCCAGTCAACGCTAGGCTGTGTGGGTGCGCTAGACCGGACCCAACTGATTG	6360
Query	6361	GACTAGTCTTGTGCTCAATTATGGCGTTAGGGACTACTGTAAATATGAGAAAATGGGAGA	6420
Sbjct	6361	GACTAGTCTTGTGCTCAATTATGGCGTTAGGGACTACTGTAAATATGAGAAAATGGGAGA	6420
Query	6421	TCACATTTTTGTTACAGCAGTATCCTCTCCAAATGTCTGTTTCACCCAGGTGCCCCAAC	6480

Sbjct	6421	TCACATCTTTGTTACAGCAGTATCCTCTCCAAATGTCTGTTTACCCAGGTGCCCCAAC	6480
Query	6481	CTTGAGAGCTGCAGTGGCCGTGGACGGCGTACAGGTTTACGTGTTATCTAGGTGAGCCCAA	6540
Sbjct	6481	CTTGAGAGCTGCAGTGGCCGTGGACGGCGTACAGGTTTACGTGTTATCTAGGTGAGCCCAA	6540
Query	6541	AACTCCTTGGACGACATCTGCTTGCTGTTACGGTCCTGACGGTAAGGGTAAAACGTGTTAA	6600
Sbjct	6541	AACTCCTTGGACGACATCTGCTTGCTGTTACGGTCCTGACGGTAAGGGTAAAACGTGTTAA	6600
Query	6601	GCTTCCCTTCCGCGTTGACGGTCACACACCTGGTGTGCGCATGCAACTTAATTTGCGTGA	6660
Sbjct	6601	GCTTCCCTTCCGCGTTGACGGTCACACACCTGGTGTGCGCATGCAACTTAATTTGCGTGA	6660
Query	6661	TGCACTTGAGACAAATGACTGTAATTCACAAACAACACTCCTAGTGATGAAGCCGCAGT	6720
Sbjct	6661	TGCACTTGAGACAAATGACTGTAATTCACAAACAACACTCCTAGTGATGAAGCCGCAGT	6720
Query	6721	GTCCGCTCTTGTTTTCAAACAGGAGTTGCGGCGTACAAACCAATTGCTTGAGGCAATTTT	6780
Sbjct	6721	GTCCGCTCTTGTTTTCAAACAGGAGTTGCGGCGTACAAACCAATTGCTTGAGGCAATTTT	6780
Query	6781	AGCTGGCGTTGACACCACCAAACCTGCCAGCCCCCTCCATCGAAGAGGTAGTGGTAAGAAA	6840
Sbjct	6781	AGCTGGCGTTGACACCACCAAACCTGCCAGCCCCCTCCATCGAAGAGGTAGTGGTAAGAAA	6840
Query	6841	GCGCCAGTTCCGGGCAAGAAGTGGTTCGCTTACCTTGCCCTCCCCCTCCGAGATCCGTCCC	6900
Sbjct	6841	GCGCCAGTTCCGGGCAAGAAGTGGTTCGCTTACCTTGCCCTCCCCCTCCGAGATCCGTCCC	6900
Query	6901	AGGAGTGTGCATGTCCTGAAAGCCTGCAACGAAGTGACCCGTTAGAAGGTCCTTCAAACCT	6960
Sbjct	6901	AGGAGTGTGCATGTCCTGAAAGCCTGCAACGAAGTGACCCGTTAGAAGGTCCTTCAAACCT	6960
Query	6961	CCCTCCTTCACCACCTGTTCTACAGTTGGCCATGCCGATGCCCTGTTGGGAGCGGGTGA	7020
Sbjct	6961	CCCTCCTTCACCACCTGTTCTACAGTTGGCCATGCCGATGCCCTGTTGGGAGCGGGTGA	7020
Query	7021	GTGTAACCCTTTCACTGCAATTGGATGTGCAATGACCGAAACAGGCGGAGGCCCTGATGA	7080
Sbjct	7021	GTGTAACCCTTTCACTGCAATTGGATGTGCAATGACCGAAACAGGCGGAGGCCCTGATGA	7080
Query	7081	TTTACCCAGTTACCCTCCCAAAAAGGAGGTCTCTGAATGGTCAGACGAAAGTTGGTTCGAC	7140
Sbjct	7081	TTTACCCAGTTACCCTCCCAAAAAGGAGGTCTCTGAATGGTCAGACGAAAGTTGGTCAAC	7140
Query	7141	GGCTACAACCGTTTCCAGCTACGTTACTGGCCCCCGTACCCTAAGATACGGGGAAAGGA	7200
Sbjct	7141	GGCTACAACCGTTTCCAGCTACGTTACTGGCCCCCGTACCCTAAGATACGGGGAAAGGA	7200
Query	7201	TTCCACTCAGTCAGCCCCGCCAAACGGCCTACAAAAAGAAGTTGGGAAAGAGTGAGTT	7260
Sbjct	7201	TTCCACTCAGTCAGCCCCGCCAAACGGCCTACAAAAAGAAGTTGGGAAAGAGTGAGTT	7260
Query	7261	TTCGTGCAGCATGAGCTACACCTGGACCGACGTGATTAGCTTCAAACTGCTTCTAAAGT	7320
Sbjct	7261	TTCGTGCAGCATGAGCTACACCTGGACCGACGTGATTAGCTTCAAACTGCTTCTAAAGT	7320
Query	7321	TCTGTCTGCAACTCGGGCCATCACTAGTGGTTTCCTCAAACAAAGATCATTGGTGTATGT	7380

Sbjct	7321	TCTGTCTGCAACTCGGGCCATCACTAGTGGTTTCCTCAAACAAAGATCATTGGTGTATGT	7380
Query	7381	GACTGAGCCGCGGGATGCGGAGCTTAGAAAACAAAAGTCACTATTAATAGACAACCTCT	7440
Sbjct	7381	GACTGAGCCGCGGGATGCGGAGCTTAGAAAACAAAAGTCACTATTAATAGACAACCTCT	7440
Query	7441	GTTCCCCCATCATACCACAAGCAAGTGAGATTGGCTAAGGAAAAAGCTTCAAAGTTGT	7500
Sbjct	7441	GTTCCCCCATCATACCACAAGCAAGTGAGATTGGCTAAGGAGAAAGCTTCAAAGTTGT	7500
Query	7501	CGGTGTCATGTGGGACTATGATGAAGTAGCAGCTCACACGCCCTCTAAGTCTGCTAAGTC	7560
Sbjct	7501	CGGTGTCATGTGGGACTATGATGAAGTAGCAGCTCACACGCCCTCTAAGTCTGCTAAGTC	7560
Query	7561	CCACATCACTGGCCTTCGGGGCACTGATGTTTCGTTCTGGAGCAGCCCGCAAGGCTGTTCT	7620
Sbjct	7561	CCACATCACTGGCCTTCGGGGCACTGATGTTTCGTTCTGGAGCAGCCCGCAAGGCTGTTCT	7620
Query	7621	GGACTTGCAGAAGTGTGTGCGAGGCAGGTGAGATACCGAGTCATTATCGGCAAACGTGAT	7680
Sbjct	7621	GGACTTGCAGAAGTGTGTGCGAGGCAGGTGAGATACCGAGTCATTATCGGCAAACGTGAT	7680
Query	7681	AGTTCCAAAGGAGGAGGTCTTCGTGAAGACCCCCAGAAACCAACAAAGAAACCCCAAG	7740
Sbjct	7681	AGTTCCAAAGGAGGAGGTCTTCGTGAAGACCCCCAGAAACCAACAAAGAAACCCCAAG	7740
Query	7741	GCTTATCTCGTACCCCCACCTTGAAATGAGATGTGTTGAGAAGATGTACTACGGTCAGGT	7800
Sbjct	7741	GCTCATCTCGTACCCCCACCTTGAAATGAGATGTGTTGAGAAGATGTACTACGGTCAGGT	7800
Query	7801	TGCTCCTGACGTAGTTAAAGCTGTCTATGGGAGATGCGTACGGGTTTGTAGATCCACGTAC	7860
Sbjct	7801	TGCTCCTGACGTAGTTAAAGCTGTCTATGGGAGATGCGTACGGGTTTGTAGATCCACGTAC	7860
Query	7861	CCGTGTCAAGCGTCTGTTGTGCGATGTGGTCACCCGATGCAGTCGGAGCCACATGCGATAC	7920
Sbjct	7861	CCGTGTCAAGCGTCTGTTGTGCGATGTGGTCACCCGATGCAGTCGGAGCCACATGCGATAC	7920
Query	7921	AGTGTGTTTTGACAGTACCATCACACCCGAGGATATCATGGTGGAGACAGACATCTACTC	7980
Sbjct	7921	AGTGTGTTTTGACAGTACCATCACACCCGAGGATATCATGGTGGAGACAGACATCTACTC	7980
Query	7981	AGCAGCTAAACTCAGTGACCAACACCGAGCTGGCATTACACCATTGCGAGGCAGTTATA	8040
Sbjct	7981	AGCAGCTAAACTCAGTGACCAACACCGAGCTGGCATTACACCATTGCGAGGCAGTTATA	8040
Query	8041	CGCTGGAGGACCGATGATCGCTTATGATGGCCGAGAGATCGGATATCGTAGGTGTAGGTC	8100
Sbjct	8041	CGCTGGAGGACCGATGATCGCTTATGATGGCCGAGAGATCGGATATCGTAGGTGTAGGTC	8100
Query	8101	TTCCGGCGTCTATACTACCTCAAGTTCCAACAGTTTGACCTGCTGGCTGAAGGTAAATGC	8160
Sbjct	8101	TTCCGGCGTCTATACTACCTCAAGTTCCAACAGTTTGACCTGCTGGCTGAAGGTAAATGC	8160
Query	8161	TGCAGCCGAACAGGCTGGCATGAAGAACCCTCGCTTCCTTATTTGCGGCGATGATTGCAC	8220
Sbjct	8161	TGCAGCCGAACAGGCTGGCATGAAGAACCCTCGCTTCCTTATTTGCGGCGATGATTGCAC	8220
Query	8221	CGTAATTTGGAAGAGCGCCGGAGCAGATGCAGACAAACAAGCAATGCGTGTCTTTGCTAG	8280

Sbjct	8221	CGTAATTTGGAAAAGCGCCGGAGCAGATGCAGACAAACAAGCAATGCGTGTCTTTGCTAG	8280
Query	8281	CTGGATGAAGGTGATGGGTGCACCACAAGATTGTGTGCCTCAACCCAAATACAGTTTGA	8340
Sbjct	8281	CTGGATGAAGGTGATGGGTGCACCACAAGATTGTGTGCCTCAACCCAAATACAGTTTGA	8340
Query	8341	AGAATTAACATCATGCTCATCAAATGTTACCTCTGGAATTACCAAAGTGGCAAGCCTTA	8400
Sbjct	8341	AGAATTAACATCATGCTCATCAAATGTTACCTCTGGAATTACCAAAGTGGCAAGCCTTA	8400
Query	8401	CTACTTTCTTACAAGAGATCCTCGTATCCCCCTTGGCAGGTGCTCTGCCGAGGGTCTGGG	8460
Sbjct	8401	CTACTTTCTTACAAGAGATCCTCGTATCCCCCTTGGCAGGTGCTCTGCCGAGGGTCTGGG	8460
Query	8461	ATACAACCCCAGTGCTGCGTGGATTGGGTATCTAATACATCACTACCCATGTTTGTGGGT	8520
Sbjct	8461	ATACAACCCCAGTGCTGCGTGGATTGGGTATCTAATACATCACTACCCATGTTTGTGGGT	8520
Query	8521	TAGCCGTGTGTTGGCTGTCCATTTTCATGGAGCAGATGCTCTTTGAGGACAAACTTCCCGA	8580
Sbjct	8521	TAGCCGTGTGTTGGCTGTCCATTTTCATGGAGCAGATGCTCTTTGAGGACAAACTTCCCGA	8580
Query	8581	GACGGTGACCTTTGACTGGTATGGGAAAAATTATACGGTGCCTGTAGAAGATCTGCCAG	8640
Sbjct	8581	GACTGTGACCTTTGACTGGTATGGGAAAAATTATACGGTGCCTGTAGAAGATCTGCCAG	8640
Query	8641	CATCATTGCTGGTGTGCACGGTATTGAGGCTTTCTCGGTGGTGCCTACACCAACGCTGA	8700
Sbjct	8641	CATCATTGCTGGTGTGCACGGTATTGAGGCTTTCTCGGTGGTGCCTACACCAACGCTGA	8700
Query	8701	GATCCTCAGAGTTTCCCAATCACTAACAGACATGACCATGCCCCCCTGCGAGCCTGGCG	8760
Sbjct	8701	GATCCTCAGAGTTTCCCAATCACTAACAGACATGACCATGCCCCCCTGCGAGCCTGGCG	8760
Query	8761	AAAGAAAGCCAGGGCGGTCTCGCCAGCGCCAAGAGGCGTGGCGGAGCACACGCAAAATT	8820
Sbjct	8761	AAAGAAAGCCAGGGCGGTCTCGCCAGCGCCAAGAGGCGTGGCGGAGCACACGCAAAATT	8820
Query	8821	GGCTCGCTTCCTTCTCTGGCATGCTACATCTAGACCTCTACCAGATTGGATAAGACGAG	8880
Sbjct	8821	GGCTCGCTTCCTTCTCTGGCATGCTACATCTAGACCTCTACCAGATTGGATAAGACGAG	8880
Query	8881	CGTGGCTCGGTACACCACTTTCAATTATTGTGATGTTTACTCCCCGAGGGGGATGTGTT	8940
Sbjct	8881	CGTGGCTCGGTACACCACTTTCAATTATTGTGATGTTTACTCCCCGAGGGGGATGTGTT	8940
Query	8941	TATTACACCACAGAGAAGATTGCAGAAGTTTCTTGTGAAGTATTTGGCTGTCATTGTTTT	9000
Sbjct	8941	TGTTACACCACAGAGAAGATTGCAGAAGTTTCTTGTGAAGTATTTGGCTGTCATTGTTTT	9000
Query	9001	TGCCCTAGGGCTCATGCTGTTGGATTAGCCATCAGCTGAACCCCAAATTCAAATTA	9060
Sbjct	9001	TGCCCTAGGGCTCATGCTGTTGGATTAGCCATCAGCTGAACCCCAAATTCAAATTA	9060
Query	9061	CTAACAGTTTTTTTTTTTTTTTTTTTTTTTTAGGGCAGCGGCAACAGGGGAGACCCGGGC	9120
Sbjct	9061	CTAACAG--TTTTTTTTTTTTTTTTTTTTTTTTAGGGCAGCGGCAACAGGGGAGACCCGGGC	9118
Query	9121	TTAACGACCCCGCCGATGTGAGTTTGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAA	9180

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Sbjct  9119  TTAACGACCCCGCCGATGTGAGTTTGGCGACCATGGTGGATCAGAACCGTTTCGGGTGAA  9178
Query  9181  GCCATGGTCTGAAGGGGATGACGTCCCTTCTGGCTCATCCACAAAACCGTCTCGGGTGG  9240
          |||
Sbjct  9179  GCCATGGTCTGAAGGGGATGACGTCCCTTCTGGCTCATCCACAAAACCGTCTCGGGTGG  9238
Query  9241  GTGAGGAGTCCTGGCTGTGTGGGAAGCAGTCAGTATAATTCCCGTCGTGTGTGGTGACGC  9300
          |||
Sbjct  9239  GTGAGGAGTCCTGGCTGTGTGGGAAGCAGTCAGTATAATTCCCGTCGTGTGTGGTGACGC  9298
Query  9301  CTCACGACGTATTTGTCCGCTGTGCAGAGCGTAGTACCAAGGGCTGCACCCCGGTTTTTG  9360
          |||
Sbjct  9299  CTCACGACGTACTTGTCCGCTGTGCAGAGCGTAGTACCAAGGGCTGCACCCCGGTTTTTG  9358
Query  9361  TTCCAAGCGGAGGGCAACCCCGCTTGAATTAAAACT  9399
          |||
Sbjct  9359  TTCCAAGCGGAGGGCAACCCCGCTTGAATTAAAACT  9397

```

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 4714
Number of extensions: 77
Number of successful extensions: 13
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 9399
Length of database: 19,583,881,279
Length adjustment: 28
Effective length of query: 9371
Effective length of database: 19,583,881,251
Effective search space: 183520551203121
Effective search space used: 183520551203121
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 16 (31.5 bits)
S2: 23 (44.9 bits)